

RAW SEQUENCE LISTING

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Application Serial Number: 101757, 473

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DATE: 03/03/2005

PATENT APPLICATION: US/10/757,473

TIME: 12:49:10

Input Set : N:\Cr3\RULE60\10757473.raw.txt

Output Set: N:\CRF4\03022005\J757473.raw

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1 <110> APPLICANT: MOECKEL, Bettina
2     BATHE, Brigitte
3     HERMANN, Thomas
4     PFEFFERLE, Walter
5     BINDER, Michael
6 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE rpoB GENE
7 <130> FILE REFERENCE: 204212US0X
8 <140> CURRENT APPLICATION NUMBER: US/10/757,473
9 <141> CURRENT FILING DATE: 2004-01-15
10 <150> PRIOR APPLICATION NUMBER: US/09/887,052
11 <151> PRIOR FILING DATE: 2001-06-25
12 <150> PRIOR APPLICATION NUMBER: DE10107229.5
13 <151> PRIOR FILING DATE: 2001-02-16
14 <160> NUMBER OF SEQ ID NOS: 8
15 <170> SOFTWARE: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 5099
19 <212> TYPE: DNA
20 <213> ORGANISM: Corynebacterium glutamicum
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (702)..(4196)
24 <400> SEQUENCE: 1
25     acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttggttgct gatctagctg      60
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27     tcgacgcctc cctcgacgat gcagctgtct ctaagctggg tgcacaggcc gaaagcatcc      180
28     ctgatggaga tgtgagcaaa atcgcaaata ccgtagggtat tgtgatcggt gcggtattgg      240
29     ctctcgtggg cctggccggg tgttttgggg cgtttgggaa gaaacgtcga gaagcttaac      300
30     ctgctgttca aatagatttt cctgtttcg aattgcggaa accccgggtt tgtttgctag      360
31     ggtgcctcgt agaaggggtc aagaagattt ctgggaaacg cgcccggtcg gttggttgct      420
32     aatagcacgc ggagcaccag atgaaaaatc tcccctttac tttcgcgcg gattggtata      480
33     ctctgagtcg ttgcgttggg attcgtgact ctttttcggt cctgtagcgc caagaccttg      540
34     atcaagggtg tttaaaaaaa ccgatttgac aaggtcattc agtgctatct ggagtcgttc      600
35     aggggggatcg ggttcctcag cagaccaatt gctcaaaaat accagcgggtg ttgatctgca      660
36     cttaatggcc ttgaccagcc aggtgcaatt acccgcgtga g  gtg  ctg  gaa  gga  ccc      716
37                                     Val Leu Glu Gly Pro
38                                     1      5
39     atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt      764
40     ile leu ala val ser arg gln thr lys ser val val asp ile pro gly
41                                     10      15      20
42     gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg      812
43     ala pro gln arg tyr ser phe ala lys val ser ala pro ile glu val
44                                     25      30      35

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45	ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt	860
46	Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly	
47	40 45 50	
48	acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc	908
49	Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala	
50	55 60 65	
51	cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc	956
52	Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile	
53	70 75 80 85	
54	cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc	1004
55	Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe	
56	90 95 100	
57	gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac	1052
58	Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn	
59	105 110 115	
60	tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc	1100
61	Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr	
62	120 125 130	
63	ggg gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg	1148
64	Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met	
65	135 140 145	
66	acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc	1196
67	Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val	
68	150 155 160 165	
69	agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat	1244
70	Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp	
71	170 175 180	
72	aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt	1292
73	Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg	
74	185 190 195	
75	ggg gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt	1340
76	Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val	
77	200 205 210	
78	cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct	1388
79	Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala	
80	215 220 225	
81	ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa	1436
82	Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu	
83	230 235 240 245	
84	atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag	1484
85	Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu	
86	250 255 260	
87	gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc	1532
88	Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr	
89	265 270 275	
90	cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag	1580
91	Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys	
92	280 285 290	
93	cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc	1628

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94	Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu	
95	295 300 305	
96	ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac	1676
97	Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp	
98	310 315 320 325	
99	atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc	1724
100	Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg	
101	330 335 340	
102	gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac	1772
103	Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro Val Glu Thr Asp Asp	
104	345 350 355	
105	atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc	1820
106	Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile	
107	360 365 370	
108	cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt	1868
109	Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg	
110	375 380 385	
111	gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg	1916
112	Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu	
113	390 395 400 405	
114	atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act	1964
115	Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr	
116	410 415 420	
117	tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg	2012
118	Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu	
119	425 430 435	
120	act cac aag cgt cgt ctg tcg gct ctg ggc ccg ggt ggt ctg tcc cgt	2060
121	Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg	
122	440 445 450	
123	gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108
124	Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly	
125	455 460 465	
126	cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156
127	Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile	
128	470 475 480 485	
129	ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204
130	Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu	
131	490 495 500	
132	acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252
133	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp	
134	505 510 515	
135	tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac	2300
136	Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn	
137	520 525 530	
138	acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348
139	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val	
140	535 540 545	
141	cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396
142	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp	

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143	550	555	560	565	
144	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg				2444
145	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met				
146		570	575	580	
147	att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg				2492
148	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala				
149		585	590	595	
150	aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc				2540
151	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe				
152		600	605	610	
153	gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg				2588
154	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu				
155		615	620	625	
156	gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc				2636
157	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe				
158		630	635	640	645
159	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt				2684
160	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg				
161		650	655	660	
162	aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg				2732
163	Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu				
164		665	670	675	
165	gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt				2780
166	Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly				
167		680	685	690	
168	cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt				2828
169	Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val				
170		695	700	705	
171	gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc				2876
172	Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu				
173		710	715	720	725
174	aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag				2924
175	Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu				
176		730	735	740	
177	gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc				2972
178	Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile				
179		745	750	755	
180	acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac				3020
181	Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp				
182		760	765	770	
183	gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc				3068
184	Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile				
185		775	780	785	
186	ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa				3116
187	Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu				
188		790	795	800	805
189	gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc				3164
190	Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg				
191		810	815	820	

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192	gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc	3212
193	Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly	
194	825 830 835	
195	gtg cgt cac ttc tcc cgc gag gac gac gac gat ctg gct cct ggc gtc	3260
196	Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val	
197	840 845 850	
198	aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac	3308
199	Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp	
200	855 860 865	
201	ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa	3356
202	Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys	
203	870 875 880 885	
204	att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt	3404
205	Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val	
206	890 895 900	
207	gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt	3452
208	Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly	
209	905 910 915	
210	cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc	3500
211	Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser	
212	920 925 930	
213	gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct	3548
214	Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro	
215	935 940 945	
216	gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg	3596
217	Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val	
218	950 955 960 965	
219	ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca	3644
220	Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser	
221	970 975 980	
222	cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca	3692
223	Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala	
224	985 990 995	
225	acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt	3737
226	Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val	
227	1000 1005 1010	
228	tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac	3782
229	Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp	
230	1015 1020 1025	
231	gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc	3827
232	Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr	
233	1030 1035 1040	
234	cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc	3872
235	Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe	
236	1045 1050 1055	
237	ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac	3917
238	Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr	
239	1060 1065 1070	
240	aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc	3962

VERIFICATION SUMMARY

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